

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: McCarthy, Sean
- (ii) TITLE OF INVENTION: NOVEL CRSP-1 COMPOSITIONS AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: FOLEY, HOAG & ELIOT LLP
  - (B) STREET: One Post Office Square
  - (C) CITY: Boston
  - (D) STATE: MA
  - (E) COUNTRY: USA
  - (F) ZIP: 02109-2170
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: US 08/842,898
  - (B) FILING DATE: 17-APR-1997
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Arnold, Beth E.
  - (B) REGISTRATION NUMBER: 35,430
  - (C) REFERENCE/DOCKET NUMBER: MAA-004.02
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 617-832-1000
  - (B) TELEFAX: 617-832-7000

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1169 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
- (A) NAME/KEY: CDS
  - (B) LOCATION: 38..1087
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCACGAGGG GGC GGCGGCT GCGGGCGCAG AGCGGAG ATG CAG CGG CTT GGG GCC 55  
Met Gln Arg Leu Gly Ala  
1 5

ACC CTG CTG TGC CTG CTG CTG GCG GCG GCG GTC CCC ACG GCC CCC GCG 103  
Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala Val Pro Thr Ala Pro Ala  
10 15 20

CCC GCT CCG ACG GCG ACC TCG GCT CCA GTC AAG CCC GGC CCG GCT CTC 151  
Pro Ala Pro Thr Ala Thr Ser Ala Pro Val Lys Pro Gly Pro Ala Leu  
25 30 35

AGC TAC CCG CAG GAG GAG GCC ACC CTC AAT GAG ATG TTC CGC GAG GTT 199  
Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn Glu Met Phe Arg Glu Val  
40 45 50

GAG GAA CTG ATG GAG GAC ACG CAG CAC AAA TTG CGC AGC GCG GTG GAA 247  
Glu Glu Leu Met Glu Asp Thr Gln His Lys Leu Arg Ser Ala Val Glu  
55 60 65 70

GAG ATG GAG GCA GAA GAA GCT GCT GCT AAA GCA TCA TCA GAA GTG AAC 295  
Glu Met Glu Ala Glu Glu Ala Ala Ala Lys Ala Ser Ser Glu Val Asn  
75 80 85

CTG GCA AAC TTA CCT CCC AGC TAT CAC AAT GAG ACC AAC ACA GAC ACG 343  
Leu Ala Asn Leu Pro Pro Ser Tyr His Asn Glu Thr Asn Thr Asp Thr  
90 95 100

AAC GTT GGA AAT AAT ACC ATC CAT GTG CAC CGA GAA ATT CAC AAG ATA 391  
Asn Val Gly Asn Asn Thr Ile His Val His Arg Glu Ile His Lys Ile  
105 110 115

ACC AAC AAC CAG ACT GGA CAA ATG GTC TTT TCA GAG ACA GTT ATC ACA 439  
Thr Asn Asn Gln Thr Gly Gln Met Val Phe Ser Glu Thr Val Ile Thr  
120 125 130

TCT GTG GGA GAC GAA GAA GGC AGA AGG AGC CAC GAG TGC ATC ATC GAC 487  
Ser Val Gly Asp Glu Glu Gly Arg Arg Ser His Glu Cys Ile Ile Asp  
135 140 145 150

GAG GAC TGT GGG CCC AGC ATG TAC TGC CAG TTT GCC AGC TTC CAG TAC 535  
Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln Phe Ala Ser Phe Gln Tyr  
155 160 165

ACC TGC CAG CCA TGC CGG GGC CAG AGG ATG CTC TGC ACC CGG GAC AGT 583  
Thr Cys Gln Pro Cys Arg Gly Gln Arg Met Leu Cys Thr Arg Asp Ser  
170 175 180

GAG TGC TGT GGA GAC CAG CTG TGT GTC TGG GGT CAC TGC ACC AAA ATG 631  
Glu Cys Cys Gly Asp Gln Leu Cys Val Trp Gly His Cys Thr Lys Met  
185 190 195

GCC ACC AGG GGC AGC AAT GGG ACC ATC TGT GAC AAC CAG AGG GAC TGC 679  
Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys Asp Asn Gln Arg Asp Cys  
200 205 210

CAG CCG GGG CTG TGC TGT GCC TTC CAG AGA GGC CTG CTG TTC CCT GTG 727  
Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg Gly Leu Leu Phe Pro Val  
215 220 225 230

TGC ACA CCC CTG CCC GTG GAG GGC GAG CTT TGC CAT GAC CCC GCC AGC 775  
 Cys Thr Pro Leu Pro Val Glu Gly Glu Leu Cys His Asp Pro Ala Ser  
 235 240 245

CGG CTT CTG GAC CTC ATC ACC TGG GAG CTA GAG CCT GAT GGA GCC TTG 823  
 Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu Glu Pro Asp Gly Ala Leu  
 250 255 260

GAC CGA TGC CCT TGT GCC AGT GGC CTC CTC TGC CAG CCC CAC AGC CAC 871  
 Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu Cys Gln Pro His Ser His  
 265 270 275

AGC CTG GTG TAT GTG TGC AAG CCG ACC TTC GTG GGG AGC CGT GAC CAA 919  
 Ser Leu Val Tyr Val Cys Lys Pro Thr Phe Val Gly Ser Arg Asp Gln  
 280 285 290

GAT GGG GAG ATC CTG CTG CCC AGA GAG GTC CCC GAT GAG TAT GAA GTT 967  
 Asp Gly Glu Ile Leu Leu Pro Arg Glu Val Pro Asp Glu Tyr Glu Val  
 295 300 305 310

GGC AGC TTC ATG GAG GAG GTG CGC CAG GAG CTG GAG GAC CTG GAG AGG 1015  
 Gly Ser Phe Met Glu Glu Val Arg Gln Glu Leu Glu Asp Leu Glu Arg  
 315 320 325

AGC CTG ACT GAA GAG ATG GCG CTG AGG GAG CCT GCG GCT GCC GCC GCT 1063  
 Ser Leu Thr Glu Glu Met Ala Leu Arg Glu Pro Ala Ala Ala Ala Ala  
 330 335 340

GCA CTG CTG GGA AGG GAA GAG ATT TAGATCTGGA CCAGGCTGTG GGTAGATGTG 1117  
 Ala Leu Leu Gly Arg Glu Glu Ile  
 345 350

CAATAGAAAT AGCTAATTTA TTTCCCCANG TGTGTGCTTT AAGCGTGGGC TG 1169

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala  
 1 5 10 15

Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val  
 20 25 30

Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn  
 35 40 45

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys  
 50 55 60

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys  
 65 70 75 80

Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn  
85 90 95

Glu Thr Asn Thr Asp Thr Asn Val Gly Asn Asn Thr Ile His Val His  
100 105 110

Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe  
115 120 125

Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser  
130 135 140

His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln  
145 150 155 160

Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met  
165 170 175

Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp  
180 185 190

Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys  
195 200 205

Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg  
210 215 220

Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu  
225 230 235 240

Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu  
245 250 255

Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu  
260 265 270

Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe  
275 280 285

Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val  
290 295 300

Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu  
305 310 315 320

Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Arg Glu  
325 330 335

Pro Ala Ala Ala Ala Ala Ala Leu Leu Gly Arg Glu Glu Ile  
340 345 350

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1050 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGCAGCGGC TTGGGGCCAC CCTGCTGTGC CTGCTGCTGG CGGCGGCGGT CCCCACGGCC 60  
 CCCGCGCCCG CTCCGACGGC GACCTCGGCT CCAGTCAAGC CCGGCCCGGC TCTCAGCTAC 120  
 CCGCAGGAGG AGGCCACCCT CAATGAGATG TTCCGCGAGG TTGAGGAACT GATGGAGGAC 180  
 ACGCAGCACA AATTGCGCAG CGCGGTGGAA GAGATGGAGG CAGAAGAAGC TGCTGCTAAA 240  
 GCATCATCAG AAGTGAACCT GGCAAACCTA CCTCCCAGCT ATCACAATGA GACCAACACA 300  
 GACACGAACG TTGGAAATAA TACCATCCAT GTGCACCGAG AAATTCACAA GATAACCAAC 360  
 AACCAGACTG GACAAATGGT CTTTTCAGAG ACAGTTATCA CATCTGTGGG AGACGAAGAA 420  
 GGCAGAAGGA GCCACGAGTG CATCATCGAC GAGGACTGTG GGCCCAGCAT GTACTGCCAG 480  
 TTTGCCAGCT TCCAGTACAC CTGCCAGCCA TGCCGGGGCC AGAGGATGCT CTGCACCCGG 540  
 GACAGTGAGT GCTGTGGAGA CCAGCTGTGT GTCTGGGGTC ACTGCACCAA AATGGCCACC 600  
 AGGGGCAGCA ATGGGACCAT CTGTGACAAC CAGAGGGACT GCCAGCCGGG GCTGTGCTGT 660  
 GCCTTCCAGA GAGGCCTGCT GTTCCCTGTG TGCACACCCC TGCCCGTGGA GGGCGAGCTT 720  
 TGCCATGACC CCGCCAGCCG GCTTCTGGAC CTCATCACCT GGGAGCTAGA GCCTGATGGA 780  
 GCCTTGGACC GATGCCCTTG TGCCAGTGGC CTCCTCTGCC AGCCCCACAG CCACAGCCTG 840  
 GTGTATGTGT GCAAGCCGAC CTTCGTGGGG AGCCGTGACC AAGATGGGGA GATCCTGCTG 900  
 CCCAGAGAGG TCCCCGATGA GTATGAAGTT GGCAGCTTCA TGGAGGAGGT GCGCCAGGAG 960  
 CTGGAGGACC TGGAGAGGAG CCTGACTGAA GAGATGGCGC TGAGGGAGCC TGCGGCTGCC 1020  
 GCCGCTGCAC TGCTGGGAAG GGAAGAGATT 1050

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Arg Gly Glu Gly Pro Ala Pro Arg Arg Arg Trp Leu Leu Leu  
 1 5 10 15  
 Leu Ala Val Leu Ala Ala Leu Cys Cys Ala Ala Ala Gly Ser Gly Gly  
 20 25 30

Arg Arg Arg Ala Ala Ser Leu Gly Glu Met Leu Arg Glu Val Glu Ala  
 35 40 45  
 Leu Met Glu Asp Thr Gln His Lys Leu Arg Asn Ala Val Gln Glu Met  
 50 55 60  
 Glu Ala Glu Glu Glu Gly Ala Lys Lys Leu Ser Glu Val Asn Phe Glu  
 65 70 75 80  
 Asn Leu Pro Pro Thr Tyr His Asn Glu Ser Asn Thr Glu Thr Arg Ile  
 85 90 95  
 Gly Asn Lys Thr Val Gln Thr His Gln Glu Ile Asp Lys Val Thr Asp  
 100 105 110  
 Asn Arg Thr Gly Ser Thr Ile Phe Ser Glu Thr Ile Ile Thr Ser Ile  
 115 120 125  
 Lys Gly Gly Glu Asn Lys Arg Asn His Glu Cys Ile Ile Asp Glu Asp  
 130 135 140  
 Cys Glu Thr Gly Lys Tyr Cys Gln Phe Ser Thr Phe Glu Tyr Lys Cys  
 145 150 155 160  
 Gln Pro Cys Lys Thr Gln His Thr His Cys Ser Arg Asp Val Glu Cys  
 165 170 175  
 Cys Gly Asp Gln Leu Cys Val Trp Gly Glu Cys Arg Lys Ala Thr Ser  
 180 185 190  
 Arg Gly Glu Asn Gly Thr Ile Cys Glu Asn Gln His Asp Cys Asn Pro  
 195 200 205  
 Gly Thr Cys Cys Ala Phe Gln Lys Glu Leu Leu Phe Pro Val Cys Thr  
 210 215 220  
 Pro Leu Pro Glu Glu Gly Glu Pro Cys His Asp Pro Ser Asn Arg Leu  
 225 230 235 240  
 Leu Asn Leu Ile Thr Trp Glu Leu Glu Pro Asp Gly Val Leu Glu Arg  
 245 250 255  
 Cys Pro Cys Ala Ser Gly Leu Ile Cys Gln Pro Gln Ser Ser His Ser  
 260 265 270  
 Thr Thr Ser Val Cys Glu Leu Ser Ser Asn Glu Thr Arg Lys Asn Glu  
 275 280 285  
 Lys Glu Asp Pro Leu Asn Met Asp Glu Met Pro Phe Ile Ser Leu Ile  
 290 295 300  
 Pro Arg Asp Ile Leu Ser Asp Tyr Glu Glu Ser Ser Val Ile Gln Glu  
 305 310 315 320  
 Val Arg Lys Glu Leu Glu Ser Leu Glu Asp Gln Ala Gly Val Lys Ser  
 325 330 335  
 Glu His Asp Pro Ala His Asp Leu Phe Leu Gly Asp Glu Ile  
 340 345 350